



STIC Biotechnology Systems Branch
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/579,104
Source: FWD
Date Processed by STIC: 5/23/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/579,104

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can **only** represent a single residue. Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220>

→ Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/579,104

DATE: 05/23/2006
TIME: 14:05:52

Input Set : A:\753-65 PCT-US Sequence Listing.txt
Output Set: N:\CRF4\05232006\J579104.raw

*Suggestion:
Consult
Sequence Rules*

3 <110> APPLICANT: POLYPHOR LTD.
5 <120> TITLE OF INVENTION: Template fixed beta-hairpin mimetics and their use in
6 phage display
8 <130> FILE REFERENCE: P1338PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,104
C--> 11 <141> CURRENT FILING DATE: 2006-05-12
13 <160> NUMBER OF SEQ ID NOS: 44
15 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

729 <210> SEQ ID NO: 43
730 <211> LENGTH: 16
731 <212> TYPE: PRT
732 <213> ORGANISM: Artificial Sequence
W--> 733 <220> FEATURE:
733 <223> OTHER INFORMATION: Cysteine residues in positions 3 and 14 are linked
734 by a disulfide bridge
E--> 736 <400> SEQUENCE: 43
W--> 737 Glu Thr Cys Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa Xaa Thr Lys
738 1 5 10 15

needs explanation
*in <220>-<223> section Does Not Comply
Corrected Diskette Needed*
<220> insert this mandatory numeric identifier
? Xaa is at position 14

*Xaa's need explanation
in <220>-<223> section*

101, 79, 104 2

SEQUENCE LISTING

replace <110> POLYPHOR LTD.

with <120> Template fixed beta-hairpin mimetics and their use in
phage display

↓ <130> P1338PCT

<1507> <140> PCT/EP 03/12783

<1517> <141> 2003-11-15

These are prior data

10/579,104 3

<210> 1
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence key sequence

<400> 1
Val Arg Lys Lys
1

insufficient
explanation - give
source

(see item 11 on
Error summary

sheet)

This type of error
appears in
subsequent
sequences, too.

10/5/99, 104 4

<210> 42
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA sequence of randomized template fixed beta-hairpin mimetic Phage library

<220>
<221> CDS
<222> (1)..(48)

<220>
<223> Xaa in the peptide chain signifies randomized amino acid positions

<220>
<223> Cysteine residues in positions 3 and 14 are linked by a disulfide bridge

<400> 42
gaa acc tgc nnk nnk nnk cgt ggt gac nnk nnk nnk thc acc aaa 48

h's need explanation in 12207-12237 section

10/579, 104 S

<210> 44

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide
for library construction

<400> 44

catgtttcg~~g~~ ccgagccacc acctttgg~~t~~ g cammmmmmm mmmngtcacc acgmmmmmm 60
~~g~~ caggttt cagagt~~g~~ a atag 84

nls need explanation

6

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/579,104

DATE: 05/23/2006
TIME: 14:05:53

Input Set : A:\753-65 PCT-US Sequence Listing.txt
Output Set: N:\CRF4\05232006\J579104.raw

Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:7; Xaa Pos. 4,5

Seq#:42; N Pos. 10,11,13,14,16,17,28,29,31,32,34,35,37,38

Seq#:42; Xaa Pos. 4,5,6,10,11,12,13,14

Seq#:43; Xaa Pos. 4,5,6,10,11,12,13,14

Seq#:44; N Pos. 34,35,37,38,40,41,43,44,55,56,58,59,61,62

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,104

DATE: 05/23/2006

TIME: 14:05:53

Input Set : A:\753-65 PCT-US Sequence Listing.txt
Output Set: N:\CRF4\05232006\J579104.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7
L:114 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
M:341 Repeated in SeqNo=42
L:733 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:736 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:43
L:737 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:43
L:737 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:43
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:752 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:44
L:752 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:44
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
M:341 Repeated in SeqNo=44